

SN 09/724910

METHODS, SYSTEMS, AND ARTICLES OF  
MANUFACTURE FOR EVALUATING  
BIOLOGICAL DATA  
ATTORNEY DOCKET No. 7414.0025

CLAIMS

3. A computer-implemented method for making correct allele calls, comprising:
- receiving a signal representing nucleic acid information;
- determining whether the signal is below a predefined complexity; and
- making an allele call for the signal based on the determination.
6. The method of any of claims 1, 3, or 4, wherein the nucleic acid information is nucleic acid length.
14. A system for making correct allele calls, comprising:
- a processor configured to execute program instructions; and
- a memory containing program instructions for execution by the processor to
- receive a signal representing nucleic acid information,
- determine whether the signal is below a predefined complexity, and
- make an allele call for the signal based on the determination.
15. The system of claim 14, wherein the nucleic acid information comprises nucleic acid length.
25. A computer readable medium containing instructions for controlling a computer system to perform a method for making correct allele calls, the method comprising:
- receiving a signal representing nucleic acid information;
- determining whether the signal is below a predefined complexity; and
- making an allele call for the signal based on the determination.

28. The method of any of claims 23, 25, or 26, wherein the nucleic acid information is nucleic acid length.

## CLAIMS

1. A computer-implemented method for making correct allele calls, comprising:  
receiving data representing nucleic acid information;  
applying at least two different allele calling algorithms to the data to provide a result for each algorithm; and  
depending on agreement between the results of each algorithm, identifying an allele call within the data and assigning a confidence level for each call.

2. The computer-implemented method of claim 1, wherein the allele calling algorithms applied in the step of applying at least two different allele calling algorithms to the data to provide a result for each algorithm are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

3. A computer-implemented method for making correct allele calls, comprising:  
receiving a signal representing nucleic acid information;  
determining whether the signal is below a predefined complexity; and  
making an allele call for the signal based on the determination.

4. A computer-implemented method for making correct allele calls, comprising:  
receiving signal representing nucleic acid information;  
applying a set of filters to the signal to eliminate peaks that do not represent alleles,

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wherein the set of filters include at least one of the following: a split peak checker; a background peak checker; a shoulder peak checker; a spike peak checker; a special peak checker; and a one basepair checker; and

determining that remaining peaks in the data are alleles after applying the set of filters to the signal.

5. The method of claim 4, wherein the applying step includes the substeps of:
- creating a list of peaks in the signal;
  - determining characteristics associated with each peak; and
  - removing peaks from the list based on the determined characteristics.

- SVB A4 6. The method of any of claims 1, 3, or 4, wherein the nucleic acid information is nucleic acid length.

7. A computer-implemented method for interpreting nucleotide or amino acid information, comprising:

- receiving data representing nucleotide or amino acid information;
- applying at least two different algorithms to the data to provide a result for each algorithm; and

- depending on agreement between the results of each algorithm, identifying at least one correct result within the data and assigning a confidence level to the at least one correct result.

8. The computer-implemented method of claim 7, wherein the algorithms applied in the step of applying at least two different algorithms to the data to provide a result for each algorithm are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

9. A computer-implemented method for making correct allele calls associated with data representing nucleic acid information, comprising:

applying each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data;

if results from all of the applied allele calling algorithms are consistent, assigning a high level of confidence for any allele calls identified in the data during application of the allele calling algorithms;

if results from all of the applied allele calling algorithms are not consistent, assigning different levels of confidence for any allele calls identified in the data during application of the allele calling algorithms depending upon which combination of the applied allele calling algorithms share consistent results; and

outputting a report including information associated with the results and any assignment of confidence levels for any allele calls identified in the data.

10. The computer-implemented method of claim 9, wherein the allele calling algorithms applied in the applying each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data, are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

11. A system for making correct allele calls, comprising:

- a processor configured to execute program instructions; and
- a memory containing program instructions for execution by the processor to
  - receive data representing nucleic acid information,
  - apply at least two different allele calling algorithms to the data to provide a result for each algorithm, and
  - depending on agreement between the results of each algorithm, identify an allele call within the data and assigning a confidence level for each call.

12. The computer-implemented method of claim 11, wherein the allele calling algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

13. The system of claim 11, wherein the nucleic acid information comprises nucleic

acid length.

14. A system for making correct allele calls, comprising:  
a processor configured to execute program instructions; and  
a memory containing program instructions for execution by the processor to  
receive a signal representing nucleic acid information,  
determine whether the signal is below a predefined complexity, and  
make an allele call for the signal based on the determination.

15. The system of claim 14, wherein the nucleic acid information comprises nucleic acid length.

16. A system for making correct allele calls, comprising:  
a processor configured to execute program instructions; and  
a memory containing program instructions for execution by the processor to  
receive signal representing nucleic acid information,  
apply a set of filters to the signal to eliminate peaks that do not represent alleles,  
wherein the set of filters include at least one of the following: a split peak checker; a background peak checker; a shoulder peak checker; a spike peak checker; a special peak checker; and a one basepair checker, and  
determine that remaining peaks in the data are alleles after applying the set of filters to the signal.





21. A system for making correct allele calls associated with data representing nucleic acid information, comprising:

a processor to execute program instructions; and

a memory that stores program instructions for execution by the processor to

apply each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data,

if results from all of the applied allele calling algorithms are consistent, assign a high level of confidence for any allele calls identified in the data during application of the allele calling algorithms,

if results from all of the applied allele calling algorithms are not consistent, assign different levels of confidence for any allele calls identified in the data during application of the allele calling algorithms depending upon which combination of the applied allele calling algorithms share consistent results, and

output a report including information associated with the results and any assignment of confidence levels for any allele calls identified in the data.

22. The system of claim 21, wherein the allele calling algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.



system to perform a method for making correct allele calls, the method comprising:

receiving signal representing nucleic acid information;

applying a set of filters to the signal to eliminate peaks that do not represent alleles, wherein the set of filters include at least one of the following: a split peak checker; a background peak checker; a shoulder peak checker; a spike peak checker; a special peak checker; and a one basepair checker; and

determining that remaining peaks in the data are alleles after applying the set of filters to the signal.

27. The computer readable medium of claim 26, wherein the applying of the set of filters includes:

creating a list of peaks in the signal;

determining characteristics associated with each peak; and

removing peaks from the list based on the determined characteristics.

28. The method of any of claims 23, 25, or 26, wherein the nucleic acid information is nucleic acid length.

29. A computer readable medium containing instructions for controlling a computer system to perform a method for interpreting nucleotide or amino acid information, the method comprising:

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allele calling algorithms depending upon which combination of the applied allele calling algorithms share consistent results; and

outputting a report including information associated with the results and any assignment of confidence levels for any allele calls identified in the data.

32. The computer readable medium of claim 31, wherein the allele calling algorithms applied in the applying of each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data, are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

33. A system for making correct allele calls, comprising:

means for receiving data representing nucleic acid information;

means for applying at least two different allele calling algorithms to the data to provide a result for each algorithm; and

means for depending on agreement between the results of each algorithm, identifying an allele call within the data and assigning a confidence level for each call.